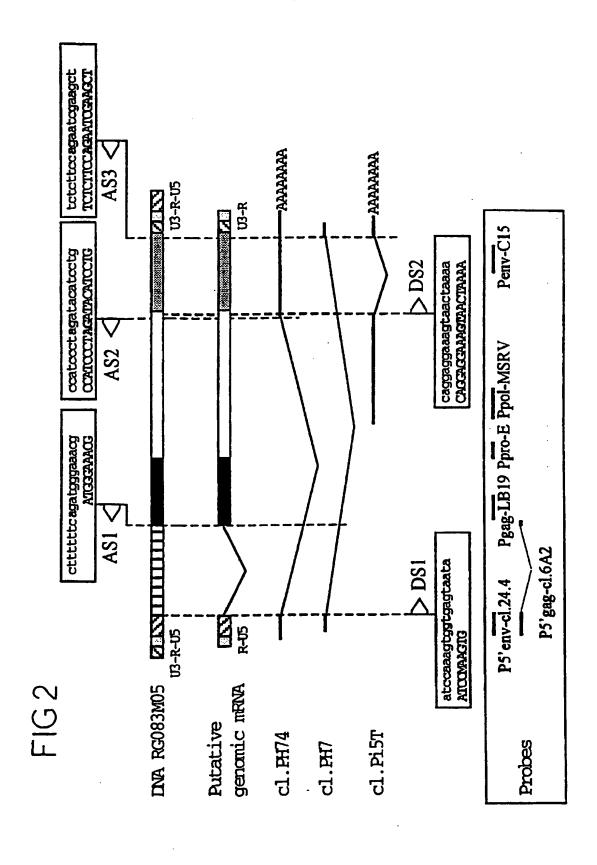


PF! 0\$4

7.7.



.φ.	<b>8</b> 2	538		413 and 305	
ORFs	538	ວິ	9	4	2
Repetitions	yes	yes	yes	yes	20
Similarities		%96	%88	89%	88%
Names	Recons RNA	RG083M05 [7]	BAC378 [14]	Q11M15[21]	U134E6 [x]
	7582	37879	14079	27999	- 94627
富]	-	28274	6911	35199	01200

3/9

FIG

## FIG 4A

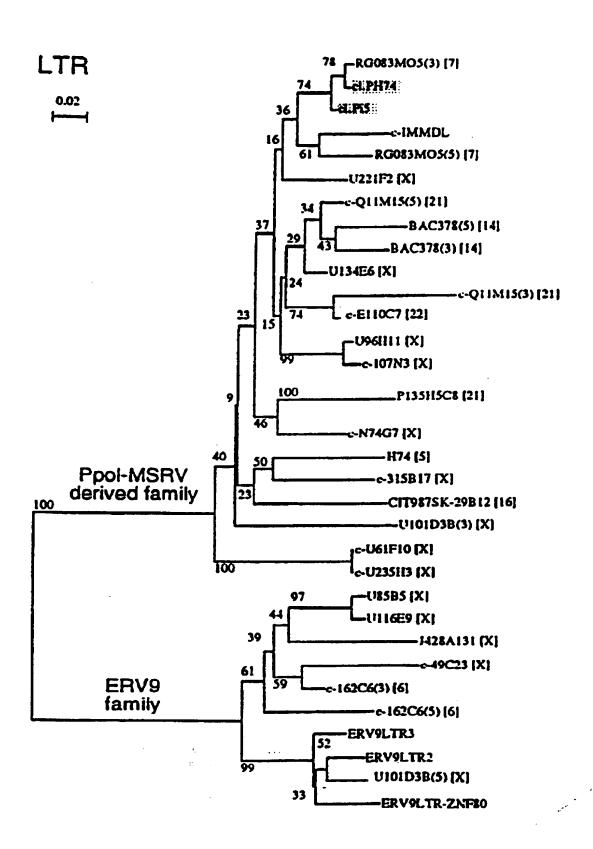
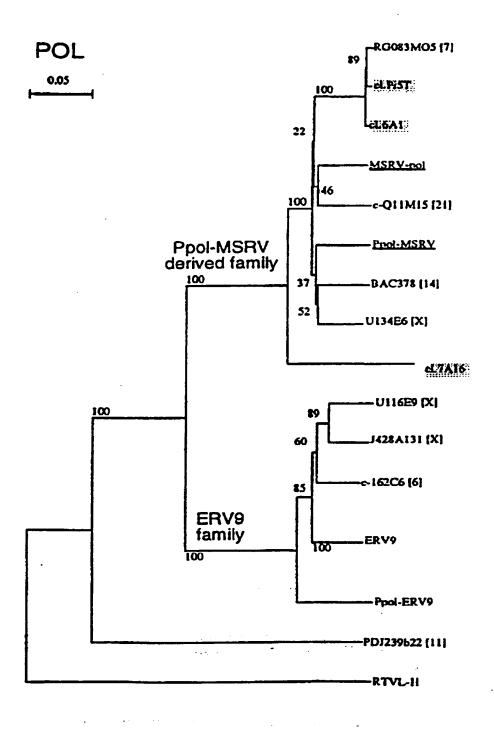
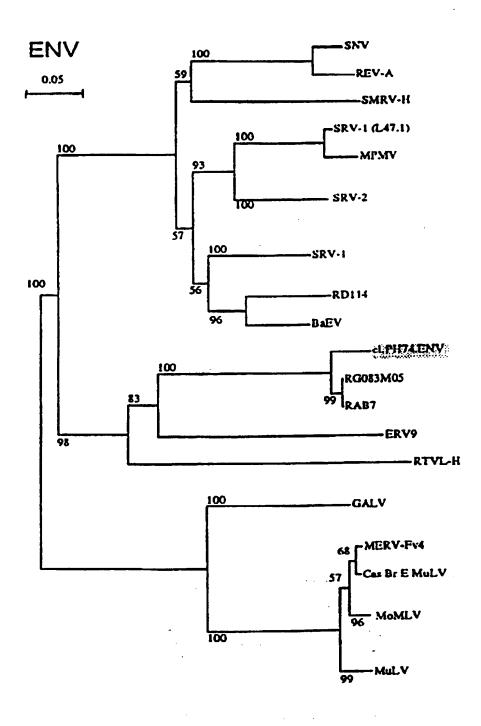


FIG 4B



## FIG 4C



# FIG 5A

5-FG-28000-28872 3-FG-37500-38314 3-FH74.2359-2782 3-C4C5.710-1136	CCCTGGGGCGGGCTTCCTTTCTGGCAAAACGCCTGGAGATACAGCAATTATCTTGCAACTGAGACAGGACTAGGATTACCTGGATTTCCTAGGCGACTAAGA  TCGTGGGCAACACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTCAGAGACTAGGATTACCTGAAAAA  C88LLC8GC8GG88GC8GLL8GAGCGTGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGGACTCAAGACTGAGAACTAGATTTCCTAAGACTAAAA  C88LLC8GC8GGB88GC8GLL8GAGCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAACAGGACTAGATTTCCTAAGACTAAAA  C88LLC8GC8GGBAGAACAGACTGCCCCCAACACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAACAGGACTGAATTTCCTAAGACTAAGA	107 93 120	
Consensus	TGAGAGACAGGACTAGCTGGATTLCTAGGCTGACTAAGA I	9	
5-RG-28000-28872 3-RG-37500-38314 3-PH74.2359-2782 3-C4C5.710-1136	ATCCCTANGCCTAGGAGGAGACCACGACCACCATAAACACGGGGGCTTGCAACTTAGCTCACCTGACCAATCAGAGGCTCACTAAAATGCTAATTAGGCAAAAGACAGAGGT ATCCCTAAGCCTAGCCGGGAAGGTGACCACACCAC	227 213 240 240	
Consensus	ATCCYTAAGCCIAGSIGGGAAGGIGACCACCTIZAACACGGGGGCTIGCAACTTAGYTCACACCTGACCAAGAGAGACTCACTBAAAAGCTAATTAGGCAAAGACAGAGGT II	160	1/9
S-RG-28000-28872 3-RG-37500-38314 3-PH74.2359-2782 3-C4C5.710-1136 5-6A2.1-600 5-PH74.1-530	AAAGAAATAGCCAATCATCTATTGCCTGAGAGGAGGGAGG	347 332 359 359 74	
Consensus	AAAGAA <u>TLAGUTATTATTOOHTGAGACACAGCAGGAGGACAAYRATCGGGAJATAA</u> CCCARGYHTTCGAGCYGGCAACRGCCCCTTTGGGTCCCTTTGTATG V	280	
5-RG-28000-28872 3-RG-37500-38314 3-PH74.2359-2782 3-C4C5.710-1136 5-GA2.1-600 5-PH74.1-530 5-24.4.1-486	GGAGCTGTTTTCATGCTALTTTCACTCTATAAATCTTGCACTCTTCTGGTCCATGTTTCTTACGGCTCGAGCTTTTGCTCACCGCCACCACCACTGTTTTGCACCACGCGCAGGGCTTTTGCTGCTCACCACTGCTGTTTTGCACCAGGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTTTTGCAGGCTGAGGCTTTTGCAGGCTGAGGCTTTTGCAGGCTGAGAGAAAAAAAA	465 452 425 427 192 121 78	

# FIG 5B

595 572 312 241 198	520	705 692 432 361	640	924 766 551 481	160	
CCGCAGACCTGCCTGACTCCCATCCCTCTGGATCCTG CCGCAGACCCGCCTGACTCCCATCCCTCTGGATCATGC CCGCAGACCTGCCTGACTCCCATCCCTTCTGAATCCTG CCGCAGACCTGCCTGACTCCCCATCCCTTGGAATCCTG CCGCAGACTGCCTGACTCCCATCCCTTGGAATCCTG	COCCANACCYGCCGCTGACTCCCCATCCCTCTGGATCHTGCAGGGTGTCCGCTGTGCTCCTGATCCAGCGARGCRCCCATTGCCGATTGGGCTTGCCATTGTTACTTGCCTTGC	ACCCCTAGENCYTOSTITOTICNALTCRACTCAACCTGGGTTCCATGGTTCTTCTTCTGTGACCCACGCTTCTAATAGAACTATAACACTTACCACATGGCCCAAGATT ATCCCTAAGTGCCTGGGTTTGTTCTAATTGAACTGAAC	-3	CCATTCCTTGGAATCCGTGAGGCCAA-GAACTCCAGGTCAGAGAE CCATTCCTTGGAATCCATAAGGCCAA-GAACCCCAGGTCAGAGAE CCATTCCTTGGAATCCGTGAGGCCAA-GAACTCCAGGTCAGAGAE CCATTCCTTGGAATCCGTGAEGCCAA-GAACTCCASGTCAGAGAE CCATTCCTTGGAATCCGTGAEGCCAA-GAACTCCAGGTCAGAGAE	CCAITCCTTGGAATCCRTRARGSCAACGAACTCCASGTCAGAGAAYACGARGCTTGCCACCATCTTGGAAGCGGCCTGCTACCATCTTGGAAGTGGTTCACCACCATCTTGGGAGCTCTG	TEACLAGEACCCCCGGTAACATTTGGCAACGACATCCA  TEAGCAAGGACCCCCCAAGTAACATTTTGGCAACACGACATCCA  TGAGCAAGGACCCCCCCAAGTAACATTTTGGCAACACCACGAACGA
5-RG-28000-28872 3-RG-37500-38314 5-6A2.1-600 5-PH74.1-530 5-24.4.1-486	Consensus	5-RG-28000-28872 3-RG-37500-38314 5-6A2.1-600 5-R74.1-530 5-24.4.1-486	Consensus	5-RG-28000-28872 3-RG-37500-38314 5-GAZ.1-600 5-PH74.1-530 5-24.4.1-486	Consensus	S-RG-28000-28872 3-RC-37500-38314 5-6A2.1-600 5-PH74.1-530 5-24.4.1-486

### ORF1: ENV (538 AA) FIG 6

<	L	><	80		
MGLPYH	IFLCSVLS	PCFTLTAPPPCR	CMTSSSPHPEFLWRMQRI	PGNIDAPSYRSLSKGTP	60
A	FT V	S	ΥQ	C	
		•			
TFTAHT	HMPRNCY	ISATLCMHANTHY1	wtgkminpscpgglgvt\	/CWTYFTQTGMSDGGGV	120
ODO 2 DE:	ひいけいせいけて で	ירו ווייים אירות ברועו	KGLDLSKLHETLRTHTRI	מפערות וביית ווייית ווייית ווייית	180
QDQAKE.	VUAVEAT5	R STIGOTOSPI	KGITI DALI TALI I VI	SV SBF WITE TO LEED VON	100
•		••	•	• *	
QNPTNC	WICLPLNE	RPYVSIPVPEQW	nnpsteinttsvlvgpl\	/SNVEITHTSNLTCVKF	240
				L	
•			•	POWOEL CELUDOWS TV	300
SMTTYT	TNSQCIRM	IA.LAB.LÖTACPAS	GIFFVCGTSAYRCLNGS	ESMC: DS: DV PFMAII	300
		>< <b>T</b> N	5	-	
TEODLY			AGVLGALGTGIGGITTS1	Pofyyklsqelngdmer	360
_					
		•		•	
VADSLV	TLQDQLNS	Laavvl <u>o</u> nrral	DLLTAERGGTCLFLGEEC		420
	•	R	S	K	
TRORTO	D T A P P T . D N	TTC DWCT.T.CDWMD	wilpflgplaaiillll	GPCIFDLLVNFVSSRI	480
		TGFMGDDSAMER	WIBIT OUT MUTE INCOME.	N	
R	·R	Õ		>	
EAVKLO	MEPKMOST	TTKTYRRPI.DRPA	SPRSDVNDIKGTPPEEIS	SAAOPLLRPNSAGSS	538

### ORF2 (52AA)

MEPKMQSKTKIYRRPLDRPVSPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS-

#### Alignment ORF2 and Rex PLLV-L

ORF2 KIY-RRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRP ++Y LD P SP ++ P S QPLLRP Rex PTLV-L (B53482) RLYNTLSLDSPPSPPKELPA----PSRFSPPQPLLRP

#### ORF3 (48AA)

MLMTSKAPLLRKSQLHNLYYAPIQQEAVRAVVGQPPQQHLGFPVEMGD

#### Alignment ORF3 and Tat SIV-AGM

ORF3 MTSKAPLLRKSQLHNLYYAPIQQEAVRAVVGQPPQ +T AP R+ ++ +L AP+Q +++ G+ Q Tat SIV-AGM(p05913) VTYHAPRTRKKIRSLNLAPLQHQSISTKWGRDGQ